Aminoacid sequence

Alignment Report of Untitled ClustalV (PAM250)
viernes, 19 de diciembre de 2008 19:38

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  1   M A E R V L T R V H S L R E R V D A T L A A H R N E I L L F L S R I E S H G K G   WT
  1   M A E R V L T R V H S L R E R V D A T L A A H R N E I L L F L S R I E S H G K G   SS5

 41   I L K P H E L L A E F D A I R Q D D K N K L N E H A F E E L L K S T Q E A I V L   WT
 41   I L K P H E L L A E F D A I R Q D D K N K L N E H A F E E[D]L K S T Q E A I V L   SS5

 81   P F W V A L A I R L R P G V W E Y I R V N V N A L V V E E L S V P E Y L Q F K E   WT
 81   P F W V A L A I R L R P G V W E Y I R V N V N A L V V E E L S V P E Y L Q F K E   SS5

121   E L V D G A S N G N F V L E L D F E P F T A S P K P T L T K S I G N G V E F L   WT
121   E L V D G A S N G N F V L E L D F E P F T A S P K P T L T K S I G N G V E F L   SS5

161   N R H L S A K M F H D K E S M T P L L E F L R A H H Y K G K T M M L N D R I Q N   WT
161   N R H L S A K M F H D K E S M T P L L E F L R A H H Y K G K T M M L N D R I Q N   SS5

201   S N T L Q N V L R K A E E Y L I M L S P D T P Y F E F E H K F Q E I G L E K G W   WT
201   S N T L Q N V L R K A E E Y L I M L S P D T P Y F E F E H K F Q E I G L E K G W   SS5

241   G D T A E R V L E M V C M L L D L L E A P D S C T L E K F L G R I P M V F N V V   WT
241   G D T A E R V L E M V C M L L D L L E A P D S C T L E K F L G R I P M V F N V V   SS5

281   I L S P H G Y F A Q E N V L G Y P D T G G Q V V Y I L D Q V P A L E R E M L K R   WT
281   I L S P H G Y F A Q E N V L G Y P D T G G Q V V Y I L D Q V P A L E R E M L K R   SS5

321   I K E Q G L D I I P R I L I V T R L L P D A V G T T C G Q R I E K V Y G A E H S   WT
321   I K E Q G L D I I P R I L I V T R L L P D A V G T T C G Q R I E K V Y G A E H S   SS5

361   H I L R V P F R T E K G I V R K W I S R F E V W P Y M E T F I E D V A K E I S A   WT
361   H I L R V P F R T E K G I V R K W I S R F E V W P Y M E T F I E D V A K E I S A   SS5

401   E L Q A K P D L I I G N Y S E G N L A A S L L A H K L G V T Q C T I A H A L E K   WT
401   E L Q A K P D L I I G N Y S E G N L A A S L L A H K L G V T Q C T I A H A L E K   SS5

441   T K Y P D S D I Y W K K F D E K Y H F S S Q F T A D L I A M N H T D F I I T S T   WT
441   T K Y P D S D I Y W K K F D E K Y H F S S Q F T A D L I A M N H T D F I I T S T   SS5

481   F Q E I A G S K D T V G Q Y E S H M A F T M P G L Y R V V H G I N V F D P K F N   WT
481   F Q E I A G S K D T V G Q Y E S H M A F T M P G L Y R V V H G I N V F D P K F N   SS5

521   I V S P G A D I N L Y F S Y S E T E K R L T A F H P E I D E L L Y S D V E N D E   WT
521   I V S P G A D I N L Y F S Y S E T E K R L T A[S]H P E I D E L L Y S D V E N D E   SS5

561   H L C V L K D R T K P I L F T M A R L D R V K N L T G L V E W Y A K N P R L R G   WT
561   H L C V L K D R T K P I L F T M A R L D R V K N L T G L V E W Y A K N P R L R G   SS5

601   L V N L V V V G G D R R K E S K D L E E Q A E M K K M Y E L I E T H N L N G Q F   WT
601   L V N L V V V G G D R R K E S K D L E E Q A E M K K M Y E L I E T H N L N G Q F   SS5

641   R W I S S Q M N R V R N G E L Y R Y I A D T K G A F V Q P A F Y E A F G L T V V   WT
641   R W I S S Q M N R V R N G E L Y R Y I A D T K G A F V Q P A F Y E A F G L T V V   SS5

681   E A M T C G L P T F A T N H G G P A E I I V H G K S G F H I D P Y H G E Q A A D   WT
681   E A M T C G L P T F A T N H G G P A E I I V H G K S G F H I D P Y H G E Q A A D   SS5

721   L L A D F F E K C K K E P S H W E T I S T G G L K R I Q E K Y T W Q I Y S E R L   WT
721   L L A D F F E K C K[R]E P S H W E T I S T[D]G L K R I Q E K Y T W Q I Y S E R L   SS5

761   L T L A A V Y G F W K H V S K L D R L E I P R Y L E M F Y A L K Y R K M A E A V   WT
761   L T L A A V Y G F W K H V S K L D R L E I P R Y L E M F Y A L K Y R K M A E A V   SS5

801   P L A A E[ ]                                                                       WT
801   P L A A E[ ]                                                                       SS5
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Nucleotide sequence

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1    ATGGCTGAACGTGTTTTGACTCGTGTTCATAGCCTTCGTG   WT
1    ATGGCTGAACGTGTTTTGACTCGTGTTCATAGCCTTCGTG   SS5

41   AACGTGTTGATGCAACTTTAGCTGCTCACCGCAATGAGAT   WT
41   AACGTGTTGATGCAACTTTAGCTGCTCACCGCAATGAGAT   SS5

81   ACTGCTGTTTCTTTCAAGGATCGAAAGCCACGGAAAAGGG   WT
81   ACTGCTGTTTCTTTCAAGGATCGAAAGCCACGGAAAAGGG   SS5

121  ATATTGAAACCTCATGAGCTTTTGGCTGAGTTCGATGCAA   WT
121  ATATTGAAACCTCA[C]GAGCTTTTGGCTGAGTTCGATGCAA   SS5

161  TTCGCCAAGATGACAAAAACAAACTGAACGAACATGCATT   WT
161  TTCGCCAAGATGACAAAAACAAACTGAACGAACATGCATT   SS5

201  CGAAGAACTCCTGAAATCCACTCAGGAAGCGATTGTTCTG   WT
201  CGAAGAAC[C]CCTGAAATCCACTCAGGAAGCGATTGTTCTG   SS5

241  CCCCCTTGGGTTGCACTTGCTATTCGTTTGAGGCCTGGTG   WT
241  CCCCCTTGGGTTGCACTTGCTATTCGTTTGAGGCCTGGTG   SS5

281  TCTGGGAATACATCCGTGTGAACGTCAATGCACTAGTTGT   WT
281  TCTGGGAATACATCCGTGTGAACGTCAATGCACTAGTTGT   SS5

321  CGAGGAG.CTGTCCGTCCCTGAGTATTTGCAATTCAAGGAA   WT
321  CGAGGAGCTGTCCGTCCCTGAGTATTTGCAATTCAAGGAA   SS5

361  GAACTTGTCGACGGAGCCTCGAATGGAAATTTTGCTCTCG   WT
361  GAACTTGTCGACGGAGCCTCGAATGGAAATTT[C]GTTCTCG   SS5

401  AGTTGGATTTCGAGCCTTTCACTGCATCCTTTCCTAAACC   WT
401  AGTTGGATTTCGAGCCTTTCACTGCATCCTTTCCTAAACC   SS5

441  AATCCTCACCAAATCTATTGGAAATGGAGTTGAATTCCTC   WT
441  AACCCTCACCAAATCTATTGGAAATGGAGTTGAATTCCTC   SS5

481  AATAGGCACCTCTCTGCCAAAATGTTCCATGACAAGGAAA   WT
481  AATAGGCACCTCTCTGCCAAAATGTTCCATGACAAGGAAA   SS5

521  GCATGACCCCGCTTCTCGAATTTCTTCGCGCTCACCATTA   WT
521  GCATGACCCCGCTTCTCGAATTTCTTCGCGCTCACCATTA   SS5

561  TAAGGGCAAGACAATGATGCTGAATGATAGGATACAGAAT   WT
561  TAAGGGCAAGACAATGATGCTGAATGATAGGATACAGAAT   SS5

601  TCGAATACTCTTCAAAATGTCCTAAGGAAGGCAGAGGAAT   WT
601  TCGAATACTCTTCAAAATGTCCTAAGGAAGGCAGAGGAAT   SS5

641  ACCTCATTATGCTTTCCCCAGATACTCCATATTTCGAATT   WT
641  ACCTCATTATGCTTTCCCCAGATACTCCATATTTCGAATT   SS5

681  CGAGCACAAGTTCCAAGAAATCGGATTGGAGAAGGGATGG   WT
681  CGAGCACAAGTTCCAAGAAATCGGATTGGAGAAGGGATGG   SS5

721  GGGGACACGGCGGAGCGTGTGCTAGAGATGGTATGCATGC   WT
721  GGGGACACGGCGGAGCGTGTGCTAGAGATGGTATGCATGC   SS5

761  TTCTTGATCTCCTTGAGGCTCCTGACTCATGTACTCTTGA   WT
761  TTCTTGATCTCCTTGAGGCTCCTGACTCATGTACTCTTGA   SS5

801  GAAGTTCTTGGGGAGAATTCCTATGGTTTTCAATGTGGTT   WT
801  GAAGTTCTTGGGGAGAATTCCTATGGTTTTCAATGTGGTT   SS5
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841   A T C C T T T C C C C T C A T G G A T A T T T T G C C C A A G A A A A T G T C T   WT
841   A T C C T T T C C C C T C A T G G A T A T T T T G C C C A A G A A A A T G T C T   SS5

881   T G G G T T A T C C C G A C A C C G G T G G C C A G G T T G T C T A C A T T T T   WT
881   T G G G T T A T C C C G A C A C C G G T G G C C A G G T T G T C T A C A T T T T   SS5

921   A G A T C A A G T T C C C G C C T T G G A G C C G T G A A A T G C T T A A G C G C   WT
921   A G A T C A A G T T C C C G C C T T G G A G C C G T G A A A T G C T T A A G C G C   SS5

961   A T A A A G G A G C A A G G A C T T G A T A T C A T C C C C C G T A T C T T A   WT
961   A T A A A G G A G C A A G G A C T T G A T A T C A T C C C C C G T A T T C T T A   SS5

1001  T T G T T A C T C G T C T G C T G C C C G A T G C A G T T G G A A C C A C T T G   WT
1001  T T G T T A C T C G T C T G C T G C C C G A T G C A G T T G G A A C C A C T T G   SS5

1041  T G G T C A G A G G A T T G A G A A G G T G T A T G G A G C A G A A C A C T C A   WT
1041  T G G T C A G A G G A T T G A G A A G G T G T A T G G A G C A G A A C A C T C A   SS5

1081  C A T A T T C T T A G G G T C C C T T T T A G G A C T G A G A A G G G C A T T G   WT
1081  C A T A T T C T T A G G G T C C C T T T T A G G A C T G A G A A G G G C A T T G   SS5

1121  T T C G C A A A T G G A T C T C T C G C T T T G A A G T G T G G C C A T A C A T   WT
1121  T T C G C A A A T G G A T C T C T C G C T T T G A A G T G T G G C C A T A C A T   SS5

1161  G G A G A C A T T C A T T G A G G A T G T T G C A A A A G A A A T T T C T G C A   WT
1161  G G A G A C A T T C A T T G A G G A T G T T G C A A A A G A A A T T T C T G C A   SS5

1201  G A A C T G C A G G C C A A G C C A G A T T T G A T A A T T G G A A A C T A C A   WT
1201  G A A C T G C A G G C C A A G C C A G A T T T G A T A A T T G G A A A C T A C A   SS5

1241  G T G A G G G C A A T C T T G C T G C T T C T T T G C T A G C T C A C A A G T T   WT
1241  G T G A G G G C A A T C T T G C T G C T T C T T T G C T A G C T C A C A A G T T   SS5

1281  A G G C G T A A C T C A G T G C A C C A T T G C C C A C G C G T T G G A G A A A   WT
1281  A G G C G T A A C T C A G T G C A C C A T T G C C C A C G C G T T G G A G A A A   SS5

1321  A C G A A G T A T C C T G A T T C C G A C A T T T A C T G G A A A A A G T T T G   WT
1321  A C G A A G T A T C C T G A T T C C G A C A T T T A C T G G A A A A A G T T T G   SS5

1361  A T G A A A A A T A C C A T T T C T C G T C C C A G T T T A C C G C T G A T C T   WT
1361  A T G A A A A A T A C C A T T T C T C G T C C C A G T T T A C C G C T G A T C T   SS5

1401  C A T T G C A A T G A A T C A C A C T G A T T T C A T C A T C A C C A G C A C C   WT
1401  C A T T G C A A T G A A T C A C A C T G A T T T C A T C A T C A C C A G C A C C   SS5

1441  T T C C A G G A G A T A G C A G G A A G C A A G G A C A C T G T A G G A C A A T   WT
1441  T T C C A G G A G A T A G C A G G A A G C A A G G A C A C T G T [C] G G A C A A T   SS5

1481  A T G A G A G C C A T A T G G C A T T C A C A A T G C C T G G A T T G T A C A G   WT
1481  A T G A G A G C C A T A T G G C A T T C A C A A T G C C T G G A T T G T A C A G   SS5

1521  A G T T G T T C A C G G C A T T A A T G T G T T C G A C C C C A A A T T C A A C   WT
1521  A G T T G T T C A [T] G G C A T T A A T G T G T T C G A C C C C A A A T T C A A C   SS5

1561  A T T G T C T C A C C T G G A G C T G A T A T T A A T C T C T A C T T C T C G T   WT
1561  A T T G T C T C A C C T G G A G C T G A T A T T A A [C] C T C T A C T T C T C G T   SS5

1601  A C T C C G A A A C G G A G A A G A G A C T T A C A G C A T T C C A C C C T G A   WT
1601  A C T C C G A A A C G G A [A] A A G A G A C T T A C A G C A T [C] C A C C C T G A   SS5

1641  A A T T G A T G A G C T G C T G T A T A G T G A T G T T G A G A A T G A C G A G   WT
1641  A A T T G A T G A G C T G C T G T A T A G T G A [C] G T T G A G A A T G A C G A [A]   SS5
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1681  C A T C T G T G T G T G C T C A A G G A C A G G A C T A A A C C A A T T T T A T  WT
1681  C A T C T G T G T G T G C T C A A G G A [T] A G G A C T A A A C C A A T T T T A T  SS5

1721  T C A C A A T G G C A A G G T T G G A T C G T G T G A A G A A T T T A A C T G G  WT
1721  T C A C A A T G G C A A G G T T G G A T C G T G T G A A G A A T T T A A C T G G  SS5

1761  A C T T G T T G A G T G G T A C G C C A A G A A T C C A C G A C T A A G G G G A  WT
1761  A C T T G T T G A G T G G T A C G C C A A G A A T C C A C G A C T A A G G G G A  SS5

1801  T T G G T T A A C C T G G T T G T A G T T G G C G G A G A T C G A A G G A A G G  WT
1801  T T G G T T A A C C T G G T T G T A G T T G G C G G A G A T C G A A G G A A G G  SS5

1841  A A T C C A A A G A T T T G G A A G A G C A G G C A G A G A T G A A G A A G A T  WT
1841  A A T C C A A A G A T T T G G A A G A G C A G G C A G A G A T G A A G A A G A T  SS5

1881  G T A T G A G C T A A T T G A G A C T C A T A A T T T G A A T G G C C A A T T C  WT
1881  G T A T G A G C T A A T [A] G A G A C T C A T A A T T T G A A T G G C C A A T T C  SS5

1921  A G A T G G A T T T C T T C C C A G A T G A A C C G A G T G A G G A A T G G T G  WT
1921  A G A T G G A T T T C T T C C C A G A T G A A C C G A G T G A G G A A T G G T G  SS5

1961  A G C T C T A C C G A T A C A T T G C T G A C A C T A A G G G A G C T T T C G T  WT
1961  A G C T C T A C C G A T A C A T T G C T G A C A C T A A G G G A G C T T T C G T  SS5

2001  T C A G C C T G C A T T C T A C G A G G C C T T T G G T C T G A C T G T T G T C  WT
2001  T C A G C C T G C A T T C T A C G A G G C [T] T T T G G T C T G A C T G T T G T C  SS5

2041  G A A G C A A T G A C T T G T G G T T T G C C T A C A T T T G C A A C T A A T C  WT
2041  G A A G C A A T G A C T T G T G G T T T G C C T A C A T T T G C A A C T A A T C  SS5

2081  A C G G T G G T C C A G C T G A G A T C A T C G T T C A T G G A A A G T C C G G  WT
2081  A C G G T G G T C C A G C T G A G A T C A T C G T T C A T G G A A A G T C C G G  SS5

2121  C T T C C A C A T T G A T C C A T A T C A C G G T G A G C A A G C T G C T G A T  WT
2121  C T T C C A C A T T G A T C C A T A T C A C G G T G A G C A A G C T G C T G A T  SS5

2161  C T G C T A G C T G A T T T C T T T G A G A A A T G C A A G A A A G A G C C T T  WT
2161  C T G C T A G C T G A T T T C T T T G A G A A A T G C A A G A [G] A G A G C C T T  SS5

2201  C A C A T T G G G A A A C C A T T T C G A C G G T G G C C T G A A G C G C A T  WT
2201  C A C A T T G G G A A A C C A T T T C G A C G G [A] T G G C C T G A A G C G C A T  SS5

2241  C C A A G A G A A G T A C A C T T G G C A A A T C T A C T C C G A A A G G C T A  WT
2241  C C A A G A G A A G T A C A C T T G G C A A A T C T A C T C C G A A A G G C T A  SS5

2281  T T G A C A C T G G C T G C T G T T T A T G G G T T C T G G A A A C A T G T T T  WT
2281  T T G A C A C T G G C T G C T G T T T A T G G G T T C T G G A A A C A T G T T T  SS5

2321  C T A A A C T T G A T C G T C T A G A A A T C C G T C G C T A T C T T G A A A T  WT
2321  C T A A [G] C T T G A T C G T C T A G A A A T C C G T C G C T A T C T T G A A A T  SS5

2361  G T T T T A T G C T C T C A A G T A C C G T A A G A T G G C T G A A G C T G T T  WT
2361  G T T T T A T G C T C T C A A G T A C C G T A A G A T G G C T G A A G C T G T T  SS5

2401  C C A T T G G C T G C T G A G T G A                                            WT
2401  C C A T T G G C T G C T G A G T G A                                            SS5
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Decoration 'Decoration #1': Shade (with solid deep red) residues that differ from SSX.